

RAW SEQUENCE LISTING DATE: 03/26/2001
 PATENT APPLICATION: US/09/424,705 TIME: 09:02:29

Input Set : A:\Pto.amc
 Output Set: N:\CRF3\03232001\I424705.raw

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4 <110> APPLICANT: LITTLE, MELVYN
5     KIPRIYANOV, SERGEY
6     MOLDENHAUER, GERHARD
7     DEUTSCHES KREBSFORSCHUNGSZEUTRUM
9 <120> TITLE OF INVENTION: MUTATED OKT3 ANTIBODY
12 <130> FILE REFERENCE: 035280047US00
14 <140> CURRENT APPLICATION NUMBER: 09/424,705
15 <141> CURRENT FILING DATE: 2000-06-02
17 <150> PRIOR APPLICATION NUMBER: PCT/DE98/01409
18 <151> PRIOR FILING DATE: 1998-05-22
20 <160> NUMBER OF SEQ ID NOS: 7
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 909
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (28)...(900)
33 <400> SEQUENCE: 1
34 gaattcatta aagaggagaa attaacc atg aaa tac cta ttg cct acg gca gcc      54
35                                     Met Lys Tyr Leu Leu Pro Thr Ala Ala
36                                     1           5
38 gct ggc ttg ctg ctg ctg gca gct cag ccg gcc atg gcg cag gtg cag      102
39 Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Gln
40 10           15           20           25
42 ctg cag cag tct ggg gct gaa ctg gca aga cct ggg gcc tca gtg aag      150
43 Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys
44           30           35           40
46 atg tcc tgc aag gct tct ggc tac acc ttt act agg tac acg atg cac      198
47 Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
48           45           50           55
50 tgg gta aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att      246
51 Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile
52           60           65           70
54 aat cct agc cgt ggt tat act aat tac aat cag aag ttc aag gac aag      294
55 Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys
56           75           80           85
58 gcc aca ttg act aca gac aaa tcc tcc agc aca gcc tac atg caa ctg      342
59 Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu
60 90           95           100          105
62 agc agc ctg aca tct gag gac tct gca gtc tat tac tgt gca aga tat      390
63 Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr
64           110          115          120
66 tat gat gat cat tac agc ctt gac tac tgg ggc caa ggc acc act ctc      438
67 Tyr Asp Asp His Tyr Ser Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu
68           125          130          135

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70  aca gtc tcc tca gcc aaa aca aca ccc aag ctt gaa gaa ggt gaa ttt      486
71  Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu Glu Glu Gly Glu Phe
72      140      145      150
74  tca gaa gca cgc gta gat atc gtg ctc act cag tct cca gca atc atg      534
75  Ser Glu Ala Arg Val Asp Ile Val Leu Thr Gln Ser Pro Ala Ile Met
76      155      160      165
78  tct gca tct cca ggg gag aag gtc acc atg acc tgc agt gcc agc tca      582
79  Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser
80  170      175      180      185
82  agt gta agt tac atg aac tgg tac cag cag aag tca ggc acc tcc ccc      630
83  Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro
84      190      195      200
86  aaa aga tgg att tat gac aca tcc aaa ctg gct tct gga gtc cct gct      678
87  Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala
88      205      210      215
90  cac ttc agg ggc agt ggg tct ggg acc tct tac tct ctc aca atc agc      726
91  His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
92      220      225      230
94  ggc atg gag gct gaa gat gct gcc act tat tac tgc cag cag tgg agt      774
95  Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser
96      235      240      245
98  agt aac cca ttc acg ttc ggc tcg ggg aca aag ttg gaa ata aac cgg      822
99  Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Asn Arg
100 250      255      260      265
102 gct gat act gca cca act gga tcc gaa caa aag ctg atc tca gaa gaa      870
103 Ala Asp Thr Ala Pro Thr Gly Ser Glu Gln Lys Leu Ile Ser Glu Glu
104      270      275      280
106 gac cta aac tca cat cac cat cac cat cac taatctaga      909
107 Asp Leu Asn Ser His His His His His His
108      285      290
111 <210> SEQ ID NO: 2
112 <211> LENGTH: 291
113 <212> TYPE: PRT
114 <213> ORGANISM: Homo sapiens
116 <400> SEQUENCE: 2
117 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
118 1 5 10 15
119 Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
120 20 25 30
121 Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
122 35 40 45
123 Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
124 50 55 60
125 Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
126 65 70 75 80
127 Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys
128 85 90 95
129 Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
130 100 105 110

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131 Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Ser Leu
132      115      120      125
133 Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr
134      130      135      140
135 Thr Pro Lys Leu Glu Glu Gly Glu Phe Ser Glu Ala Arg Val Asp Ile
136 145      150      155      160
137 Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys
138      165      170      175
139 Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
140      180      185      190
141 Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr
142      195      200      205
143 Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser
144      210      215      220
145 Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala
146 225      230      235      240
147 Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly
148      245      250      255
149 Ser Gly Thr Lys Leu Glu Ile Asn Arg Ala Asp Thr Ala Pro Thr Gly
150      260      265      270
151 Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser His His His
152      275      280      285
153 His His His
154      290
156 <210> SEQ ID NO: 3
157 <211> LENGTH: 906
158 <212> TYPE: DNA
159 <213> ORGANISM: Homo sapiens
161 <220> FEATURE:
162 <221> NAME/KEY: CDS
163 <222> LOCATION: (28)...(897)
165 <400> SEQUENCE: 3
166 gaattcatta aagaggagaa attaacc atg aaa tac cta ttg cct acg gca gcc      54
167      Met Lys Tyr Leu Leu Pro Thr Ala Ala
168      1      5
170 gct ggc ttg ctg ctg ctg gca gct cag ccg gcc atg gcg cag gtg cag      102
171 Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Gln
172 10      15      20      25
174 ctg cag cag tct ggg gct gaa ctg gca aga cct ggg gcc tca gtg aag      150
175 Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys
176      30      35      40
178 atg tcc tgc aag gct tct ggc tac acc ttt act agg tac acg atg cac      198
179 Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
180      45      50      55
182 tgg gta aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att      246
183 Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile
184      60      65      70
186 aat cct agc cgt ggt tat act aat tac aat cag aag ttc aag gac aag      294
187 Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys

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188      75      80      85
190 gac aag gcc aca ttg act aca gac aaa tcc tcc agc aca gcc tac atg      342
191 Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met
192 90      95      100      105
194 caa ctg agc agc ctg aca tct gag gac tct gca gtc tat tac tgt gca      390
195 Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
196      110      115      120
198 aga tat tat gat gat cat tac agc ctt gac tac tgg ggc caa ggc acc      438
199 Arg Tyr Tyr Asp Asp His Tyr Ser Leu Asp Tyr Trp Gly Gln Gly Thr
200      125      130      135
202 act ctc aca gtc tcc tca gcc aaa aca aca ccc aag ctt ggc ggt gat      486
203 Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu Gly Gly Asp
204      140      145      150
206 atc ttg ctc acc caa act cca gct tct ttg gct gtg tct cta ggg cag      534
207 Ile Leu Leu Thr Gln Thr Pro Ala Ser Leu Ala Val Ser Leu Gly Gln
208      155      160      165
210 agg gcc acc atc tcc tgc aag gcc agc caa agt gtt gat tat gat ggt      582
211 Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly
212 170      175      180      185
214 gat agt tat ttg aac tgg tac caa cag att cca gga cag cca ccc aaa      630
215 Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys
216      190      195      200
218 ctc ctc atc tat gat gca tcc aat cta gtt tct ggg atc cca ccc agg      678
219 Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg
220      205      210      215
222 ttt agt ggc agt ggg tct ggg aca gac ttc acc ctc aac atc cat cct      726
223 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro
224      220      225      230
226 gtg gag aag gtg gat gct gca acc tat cac tgt cag caa agt act gag      774
227 Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu
228      235      240      245
230 gat ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa cgg gct      822
231 Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala
232 250      255      260      265
234 gat gct gcg gcc gct gga tcc gaa caa aag ctg atc tca gaa gaa gac      870
235 Asp Ala Ala Ala Ala Gly Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp
236      270      275      280
238 cta aac tca cat cac cat cac cat cac taaagatct      906
239 Leu Asn Ser His His His His His
240      285      290
243 <210> SEQ ID NO: 4
244 <211> LENGTH: 290
245 <212> TYPE: PRT
246 <213> ORGANISM: Homo sapiens
248 <400> SEQUENCE: 4
249 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
250 1      5      10      15
251 Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
252      20      25      30

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```

253 Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
254      35      40      45
255 Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
256      50      55      60
257 Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
258 65      70      75      80
259 Asn Tyr Asn Gln Lys Phe Lys Asp Lys Asp Lys Ala Thr Leu Thr Thr
260      85      90      95
261 Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser
262      100     105     110
263 Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr
264      115     120     125
265 Ser Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala
266      130     135     140
267 Lys Thr Thr Pro Lys Leu Gly Gly Asp Ile Leu Leu Thr Gln Thr Pro
268 145     150     155     160
269 Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys
270      165     170     175
271 Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr
272      180     185     190
273 Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser
274      195     200     205
275 Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly
276      210     215     220
277 Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala
278 225     230     235     240
279 Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly
280      245     250     255
281 Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Ala Ala Gly Ser
282      260     265     270
283 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser His His His His
284      275     280     285
285 His His
286      290
288 <210> SEQ ID NO: 5
289 <211> LENGTH: 900
290 <212> TYPE: DNA
291 <213> ORGANISM: Homo sapiens
293 <220> FEATURE:
294 <221> NAME/KEY: CDS
295 <222> LOCATION: (28)...(891)
297 <400> SEQUENCE: 5
298 agatctatta aagaggagaa attaaccc atg aaa tac cta ttg cct acg gca gcc      54
299      Met Lys Tyr Leu Leu Pro Thr Ala Ala
300      1      5
302 gct ggc ttg ctg ctg ctg gca gct cag ccg gcc atg gcg cag gtg cag      102
303 Ala Gly Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Gln
304 10      15      20      25
306 ctg cag cag tct ggg gct gag ctg gtg agg cct ggg tcc tca gtg aag      150

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VERIFICATION SUMMARY

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